

SEQUENCE LISTING

<110> Poch, Jean-Marc
Bartel, Paul L.
Heichman, Karen

<120> Protein-Protein Interactions in Neurodegenerative
Diseases

<130> Protein Interactions in ND

<140>

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<150> US 60/240,790

<151> 2000-10-17

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<170> PatentIn Ver. 2.0

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:tail for
forward primer for yeast two-hybrid system

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gcaggaaaca gatatgacca tacagtca ggcggccacc

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<223> Description of Artificial Sequence:tail for
reverse primer for yeast two-hybrid system

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acggccatc ggtggagtg ttatgtcatg cggccgta

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taattaaaaac attttcagg gacgtaccca tccagagaca ttccattatt gttccattga 180

cctttccctc atcactgagt ctttgaggc tgatgtt atg tca aca gct gcc tta 234

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att act ttg gtc aga agt ggt ggg aac cag gtg aga agg aga gtg ctg						282
Ile Thr Leu Val Arg Ser Gly Gly Asn Gln Val Arg Arg Arg Val Leu	10	15			20	
ctc agc tcc cgc ctg ctg cag gag gac agg cgg gtg aca ccc acg tgc						330
Leu Ser Ser Arg Leu Leu Gln Asp Asp Arg Arg Val Thr Pro Thr Cys	25	30		35		
cac agc tcc act tca gag cct agg tgg tct cgg ttt gac cca gat ggt						378
His Ser Ser Thr Ser Glu Pro Arg Cys Ser Arg Phe Asp Pro Asp Gly	40	45		50		
agt ggg agt cca gct acc tgg gac aat ttt ggg atc tgg gat aac cgc						426
Ser Gly Ser Pro Ala Thr Trp Asp Asn Phe Gly Ile Trp Asp Asn Arg	55	60		65		
att gat gag cca att ctg ctg cca ccc agc att aag tat ggc aag cca						474
Ile Asp Glu Pro Ile Leu Leu Pro Pro Ser Ile Lys Tyr Gly Lys Pro	75		80		85	
att ccc aaa atc agc ttg gaa aat gtg ggg tgc gcc tca cag att ggc						522
Ile Pro Lys Ile Ser Leu Glu Asn Val Gly Cys Ala Ser Gln Ile Gly	90		95		100	
aaa cgg aaa gag aat gaa gat cgg ttt gac ttc gct cag ctg aca gat						570
Lys Arg Lys Glu Asn Glu Asp Arg Phe Asp Phe Ala Gln Leu Thr Asp	105		110		115	
gag gtc ctg tac ttt gca gtg tat gat gga cac ggt gga cct gca gca						618
Glu Val Leu Tyr Phe Ala Val Tyr Asp Gly His Gly Gly Pro Ala Ala	120		125		130	
gtc gat ttc tgt cat acc cac atg gag aaa tgt att atg gat ttg ctt						666
Ala Asp Phe Cys His Thr His Met Glu Lys Cys Ile Met Asp Leu Leu	135		140		145	
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cct aag gag aag aac ttg gaa act ctg ttg acc ttg gct ttt cta gaa						714
Pro Lys Glu Lys Asn Leu Glu Thr Leu Leu Thr Leu Ala Phe Leu Glu	155		160		165	
ata gat aaa gcc ttt tgg agt cat gcc cgc ctg tct gct gat gca act						762
Ile Asp Lys Ala Phe Ser Ser His Ala Arg Leu Ser Ala Asp Ala Thr	170		175		180	
ctt ctg acc tct ggg act act gca aca gta gcc cta ttg cga gat ggt						810
Leu Leu Thr Ser Gly Thr Thr Ala Thr Val Ala Leu Leu Arg Asp Gly	185		190		195	
att gaa ctg gtt gta gcc agt gtt ggg gag aac cgg gct att ttg tgt						858
Ile Glu Leu Val Val Ala Ser Val Gly Asp Ser Arg Ala Ile Leu Cys	200		205		210	
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aga aaa gga aaa ccc atg aag ctg aca att gag cat act cca gaa aga						906
Arg Lys Gly Lys Pro Met Lys Leu Thr Ile Asp His Thr Pro Glu Arg	220		225		230	
aaa gat gaa aaa jaa agg atc aag aaa tgt ggt ggt ttt gta gct tgg						954
Lys Asp Glu Lys Glu Arg Ile Lys Lys Cys Gly Gly Phe Val Ala Trp	235		240		245	
aat agt ttg ggg cag cct cac gta aat ggc agg ctt gca atg aca aga						1002

Asn Ser Leu Gly Gln Pro His Val Asn Gly Arg Leu Ala Met Thr Arg			
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agt att gga gat ttg gac ctt aag acc agt ggt gtc ata gca gaa cct		1050	
Ser Ile Gly Asp Leu Asp Leu Lys Thr Ser Gly Val Ile Ala Glu Pro			
265	270	275	
gaa act aag agg att aag tta cat cat gct gat gac agc ttc ctg gtc		1098	
Glu Thr Lys Arg Ile Lys Leu His His Ala Asp Asp Ser Phe Leu Val			
280	285	290	
ctc acc aca gat gga att aac ttc atg gtg aat agt caa gag att tgt		1146	
Leu Thr Thr Asp Gly Ile Asn Phe Met Val Asn Ser Gln Glu Ile Cys			
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gac ttt gtc aat cag tgc cat gat ccc aac gaa gca gcc cat gcg gtg		1194	
Asp Phe Val Asn Gln Cys His Asp Pro Asn Glu Ala Ala His Ala Val			
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act gaa cag gca ata cag tac ggt act gag gat aac agt act gca gta		1242	
Thr Glu Gln Ala Ile Gln Tyr Gly Thr Glu Asp Asn Ser Thr Ala Val			
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Val Val Pro Phe Gly Ala Trp Gly Lys Tyr Lys Asn Ser Glu Ile Asn			
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Phe Ser Phe Ser Arg Ser Phe Ala Ser Ser Gly Arg Trp Ala			
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 35 40 45
 Arg Phe Asp Pro Asp Gly Ser Gly Ser Pro Ala Thr Trp Asp Asn Phe
 50 55 60
 Gly Ile Trp Asp Asn Arg Ile Asp Glu Pro Ile Leu Leu Pro Pro Ser
 65 70 75 80
 Ile Lys Tyr Gly Lys Pro Ile Pro Lys Ile Ser Leu Glu Asn Val Gly
 85 90 95
 Cys Ala Ser Gln Ile Gly Lys Arg Lys Glu Asn Glu Asp Arg Phe Asp
 100 105 110
 Phe Ala Gln Leu Thr Asp Glu Val Leu Tyr Phe Ala Val Tyr Asp Gly
 115 120 125
 His Gly Gly Pro Ala Ala Ala Asp Phe Cys His Thr His Met Glu Lys
 130 135 140
 Cys Ile Met Asp Leu Leu Pro Lys Glu Lys Asn Leu Glu Thr Leu Leu
 145 150 155 160
 Thr Leu Ala Phe Leu Glu Ile Asp Lys Ala Phe Ser Ser His Ala Arg
 165 170 175
 Leu Ser Ala Asp Ala Thr Leu Leu Thr Ser Gly Thr Thr Ala Thr Val
 180 185 190
 Ala Leu Leu Arg Asp Gly Ile Glu Leu Val Val Ala Ser Val Gly Asp
 195 200 205
 Ser Arg Ala Ile Leu Cys Arg Lys Gly Lys Pro Met Lys Leu Thr Ile
 210 215 220

Asp His Thr Pro Glu Arg Lys Asp Glu Lys Glu Arg Ile Lys Lys Cys
225 230 235 240

Gly Gly Phe Val Ala Trp Asn Ser Leu Gly Gln Pro His Val Asn Gly
245 250 255

Arg Leu Ala Met Thr Arg Ser Ile Gly Asp Leu Asp Leu Lys Thr Ser
260 265 270

Gly Val Ile Ala Glu Pro Glu Thr Lys Arg Ile Lys Leu His His Ala
275 280 285

Asp Asp Ser Phe Leu Val Leu Thr Thr Asp Gly Ile Asn Phe Met Val
290 295 300

Asn Ser Gln Glu Ile Cys Asp Phe Val Asn Gln Cys His Asp Pro Asn
305 310 315 320

Glu Ala Ala His Ala Val Thr Glu Gln Ala Ile Gln Tyr Gly Thr Glu
325 330 335

Asp Asn Ser Thr Ala Val Val Val Pro Phe Gly Ala Trp Gly Lys Tyr
340 345 350

Lys Asn Ser Glu Ile Asn Phe Ser Phe Ser Arg Ser Phe Ala Ser Ser
355 360 365

Gly Arg Trp Ala
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